

Appendix 2 (as supplied by the authors): Markov Chain Model for Initial Wave of Pandemic Influenza A (H1N1) in Ontario

Initial cases can be categorized as those that were imported to Ontario from source regions with local transmission (believed to be Mexico) (I_{Import}), and those cases that were acquired via local transmission (I_{Local}). A simple state transition model with disease transmission is:

$$\frac{dE}{dt} = R_0 \gamma (I_{Local} + I_{Import}) - \varepsilon E \quad (A2.1)$$

$$\frac{dI}{dt} = \varepsilon E + I_{Import} - \gamma (I_{Local} + I_{Import}) \quad (A2.2)$$

$$\frac{dR}{dt} = \gamma (I_{Local} + I_{Import}) \quad (A2.3)$$

where E and R represent those exposed (but not yet infectious) and recovered, respectively. R_0 is the basic reproductive number (equal to the product of three parameters: probability of transmission per contact, number of contacts, and duration of infectiousness), $1/\varepsilon$ is the latent period, and (as in Appendix 1 above), γ is the rate of recovery from infection (such that $1/\gamma$ is the average duration of infectiousness). Model parameters were estimated iteratively using best-fit algorithms, as described in the text.